

EXHIBIT A

Sequence alignment (SEQ ID NO:1 top and SEQ ID NO:3 bottom)

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>_                                     861 nt vs.
>_                                     796 nt
scoring matrix: , gap penalties: -12/-2
92.0% identity;      Global alignment score: 3006

      10      20      30      40      50      60
935757 ATGAACAAGTTGAAATCATCGCAGAAGGATAAAGTTCGTCAGTTTATGATCTTCACACAA
      :
_      -----CGTCAGTTTATGATCTTCACACAA
                        10      20

      70      80      90     100     110     120
935757 TCTAGTGAAAAACAGCAGTAAGTTGTCTTTCTCAAATGACTGGAAGTTAGATGTTGCA
      :
_      TCTAGTGAAAAACAGCAGTAAGTTGTCTTTCTCAAATGACTGGAAGTTAGATGTTGCA
      30      40      50      60      70      80

      130     140     150     160     170     180
935757 ACAGATAATTTTTTCCAAAATCCTGAACTTTATATACGAGAGAGTGTAAGGATCATTG
      :
_      ACAGATAATTTTTTCCAAAATCCTGAACTTTATATACGAGAGAGTGTAAGGATCATTG
      90     100     110     120     130     140

      190     200     210     220     230     240
935757 GACAGGAAGAAGTTAGAACAGCTGTACAATAGATACAAAGACCCTCAAGATGAGAATAAA
      :
_      GACAGGAAGAAGTTAGAACAGCTGTACAATAGATACAAAGACCCTCAAGATGAGAATAAA
      150     160     170     180     190     200

      250     260     270     280     290     300
935757 ATTGGAATAGATGGCATAACAGCAGTTCTGTGATGACCTGGCACTCGATCCAGCCAGCATT
      :
_      ATTGGAATAGATGGCATAACAGCAGTTCTGTGATGACCTGGCACTCGATCCAGCCAGCATT
      210     220     230     240     250     260

      310     320     330     340     350     360
935757 AGTGTGTTGATTATTGCGATGGAAGTTTCAGAGCAGCAACACAGTGCGAGTTCTCCAAACAG
      :
_      AGTGTGTTGATTATTGCGTGAAGTTTCAGAGCAGCAACACAGTGCGAGTTCTCCAAACAG
      270     280     290     300     310     320

      370     380     390     400     410     420
935757 GAGTTCATGGATGGCATGACAGAATTAGGATGTGACAGCATAGAAAACTAAAGGCCAG
      :
_      GAGTTCATGGATGGCATGACAGAATTAGGATGTGACAGCACAGAAAACTAAAGGCCAG
      330     340     350     360     370     380

      430     440     450     460     470     480
935757 ATACCCAAGATGGAACAAGAATTGAAAGAACCAGGACGATTTAAGGATTTTACCAGTTT
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-          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
          ATACCCAAGATGGAACAAGAATTGAAAGAACCAGGACGATTTAAGGATTTTACCAGTTT
          390      400      410      420      430      440

          490      500      510      520      530      540
935757 ACTTTTAATTTTGCAAAGAATCCAGGACAAAAAGGATTAGATCTAGAAATGGCCATTGCC
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
-          ACTTTTAATTTTGCAAAGAATCCAGGACAAAAAGGATTAGATCTAGAAATGGCCATTGCC
          450      460      470      480      490      500

          550      560      570      580      590      600
935757 TACTGGAACCTTAGTGCTTAATGGAAGATTTAAATTCTTAGACTTATGGAATAAATTTTGT
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
-          TACTGGAACCTTAGTGCTTAATGGAAGATTTAGACTCTTAGACTTATGGAATAAATTTTGT
          510      520      530      540      550      560

          610      620      630      640      650      660
935757 TTGGAACATCATAAACGATCAATACCAAAAGACACTTGGAATCTTCTTTTAGACTTCAGT
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
-          TTGGAACATCATAAACGATCAATACCAAAAGACACTTGGAATCTTCTTTTAGACTTCAGT
          570      580      590      600      610      620

          670      680      690      700      710      720
935757 ACGATGATTGCAGATGACATGTCTAATTATGATGAAGAAGGAGCATGGCCTGTTCTTATT
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
-          ACGATGATTGCAGATGACATGTCTAATTATGATGAAGAAGGAGCATGGCCTGTTCTTATT
          630      640      650      660      670      680

          730      740      750      760      770      780
935757 GATGACTTTGTGGAATTTGCACGCCCTCAAATTGCTGGGACAAAAAGTACAACAGTGTAG
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
-          GATGACTTTGTGGAATTTGCACGCCCTCAAATTGCTGGGACAAAAAGTACAACAGTGTAG
          690      700      710      720      730      740

          790      800      810      820      830      840
935757 CACTAAAGGAACCTTCTAGAATGTACATAGTCTGTACAATAAATACAACAGAAAATTGCA
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
-          CACTAAAGGAACCTTCTAGAATGTACATAGTCTGTACAATAAATACAACAGA-----
          750      760      770      780      790

          850      860
935757 CAGTCAATTTCTGCTGGCTGG
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Elapsed time: 0:00